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TCGACCCACGCGTCCGGGAGGATCGGGAGTCCGGGAGGATGGGCCGCGCTAGGCTCGCACTCCGGA
CGCGCCTCGC
AGTGCAGAGGTGGGTGCCCCGCGCCTGCAGCGTCCGCCGGGGCGGCGCGGCGGGAGGTGGCCGACAG
GCTCCGGGCC
TCGCAGCCTCAGCCCCCGGCCAGCGCGCTTTCCGACGGCGGCGCGCGCCGAGCCACCCGCC
CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAACCTCCCAACTTCCTGAGTTCTAAAGTTCCTGTTG
CTTCAGACAA
TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCTCAGTTCCAACCACAGAAGGCCTTACGA
CCGGATATGG
GCTATAATACATTAGCCAACTTTTGAATAGAAAAGAAAATTGGTTCGCGGACAATTTAGTGAAG
TTTATAGAGCAGCCTGTCTCTTGGATGGAGTACCAGTAGCTTTAAAAAAGTGCAGATATTTGATTTA
ATGGATGCCA
AAGCACGTGCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
TATTATGCAT
CATTCATTGAAGATAATGAACTAAACATAGTTTTTGGAACTAGCAGATGCTGGCGACCTATCCA
GAATGATCAAGCATTTTAAGAAGCAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAAGTATTTGTT
CAGCTTTGCA
GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTTATT
ACAGCCACTG
GGGTGGTAAAACTTGGAGATCTTGGGCTTGGCCGGTTTTTTCAGCTCAAAAACACAGCTGCAC
ATTCTTTAGTTGGTACGCCTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACCTCAA
TCTGACATCT
GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
TTATACTCAC
TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTTCAGATCACTATTGAGAAGAAC
TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAAGCGACCAGACGTACCTATGTTTAT
GACGTAGCAA
AGAGGATGCATGCATGCACTGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGTAACCAAAGTAATT
GAAAGTATTT
TGTGCAAAGTCGTACCTSCCCATTTATGTCTGGGTGTTAAGATTAATATTTTCAGAGCTAGTGT
GCTCTGAATCCTTAACCAGTTTTTCATATAAGCTTCATTTTGTACCAGTCACCTAAATCACCTCCTTGC
AACCCCCAAA
TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
GTTTATAGAA
TTTCTTACAGTTTTCTGCTGATAAATTGTGTTTAGATAGACTGTCAGTGCCAAATATTGAAGG
TGCAGCTTGGCACACATCAGAATAGACTCATACCTGAGAAAAAGTATCTGAACATGTGACTTGTCTCT
TTTTTAGTAA
TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTTAAACGTTTGAAGTA
CTAGTTTTAG
TTCCTAGCAGAGTAGTTTTCAAATATGATTCTTATGATAAATGTAGACACAACTATTTGAGA
AACATTTAGAAGCTTTAGCTTATACATTCAAATGTAAGTATTAAATGTGAAGATTGGGGACAAAAT
GTGAGTCAGA
CACTGAAGAGTTTTTTGTTTTGTTTTAATATTTTTGATATTCTCTTTCATTGAAATGGTATAAATGA
ATCCATTTAA
AAAGTGGTTAAGGATTTGTTTAGCTGGTGTGATAATAATTTTTAAAGTTGCACATTGCCCAAG
GCTTTTTTTGTGTGTTTTATTGTTGTTGTACATTTGAAAAATATTCTTTGAATAACCTTGCAGTAC
TATATTTCAA

FIGURE 1

TTTCTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTATT
CATAAGTTTT
ATTGAAGTTCTGATCGGTCCCCCTTCAGAAATTTTTTTTATATTATTCTTCAAGTTACTTTCTTA
TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
GATATTTGGT
ATACCAATACTTTTTCTGGATTGAAAACTTTTTTTAACTTTTTTAAAATTTGGGCCACTCTGTATGCA
TATGTTTGGT
CTTGTTAAAGAGGAAGAAAGGATGTGTGTTATACTGTACCTGTGAATGTTGATACAGTTACAA
TTTATTTGACAAGGTTGTAATTCTAGAATATGCTTAATAAAATGAAAACCTGGCCATGACTACAGCCAG
AACTGTTATG
AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTTCATGAAGATGACTGAGATG
GTAACACTTC
GTGTAGCTTAAGGAAATGGGCAGAATTTTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
TGCTTTTCGTATTAGTGCGCACCAGTTTCTCACAGAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCACT
GTTAAAGGAC
TCTGTGCCATCTTACAACCTTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
TCCCTTTAGC
CGATGTAAGTGTGTTTGTGTTTTCATATGTGTTTCTTACACTCATTTGAATGCTTTCAA
GCATTTGTAACTTAAAAAANWAWAAAGGGCAAAAAGTCTGAACCCTGTGTTTCTGAAATCTAATC
AGTTATGTAT
GGTTTCTGAAGGGTAATTTTATTTTGAATAGGTAAAGCGAAACCTGTTTGTGTCGTTGTTTTCTGAG
GGCTAGATGC
ATTTTTTTTCTCACACTCTTAATGACTTTTAACATTTATACTGAGCATCCATAGATATATTCC
TAGAAGTATGAGAAGAATTATTCTTATTGACCATTAATGTATGTTTCAATTTAATGTAATATAATTGA
GATGAAATGT
TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
ATTAGCTTGA
CCCCTCAAAGTAACTTTTAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAAATTCATTATTTCTATATGTGGAACTTTTTGCT
TCGAATATTG
TATCTTTTTAAATCTAAATGTTTCATATTTTCTGAAGAAACCACTGTGTAAAAATCAAATTTTAATT
TTGAATGGAA
TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
CTTTATATGTGTTTATAAGTAAATTTTATATTGATTAAGTTAACTTTTGAATTGATTTGAGGAGCAG
TAAAATGAAA
GCTATATCTATTNCTAAACCYTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
TTGTTTTGTA
TGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAATAAAGTGCTCAACAATGTG
CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTATGAATGCTTTACCATTCAACATAGTATCT
ATTACAAAAC
ACCTTTCTGTATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAA
ATGTTACTCA
CATTAAATGTTTATTTCTTTAAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTGTGAAATACTTTTATTTTGTATGC
TTTAAATATA
CATACAAAAGATTTCTGTTATTAGCTTTGAAAATTTGTATAATATCCTAATATAAACAAAATATAAA
AATAAAATG
AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAAGG

FIGURE 1 (cont'd)

MDEQSQGMQGPVPVQFQPQKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYFVQLC
SALEHMHSRR
VMHRDIKPANVFITATGVVVLGDLGLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLVSLCKKIEQCDYPPLPSDHYSEELRQLVNMCIINPDPEKRPDVTY
VYDVAKRMHA
CTASS

FIGURE 1 (cont'd)

GTCGACCCACGCGTCCGGTGGAAGTATAATACTTTGTCTATTATGAGATGTCGTCTCTCGG
TGCTCTCTTTGTGCAAATTAAATTTGATGACTTGACGTTTTTTTGAAAACCTGCGGTGGAGG
AAGTTTTGGGAGTGTATATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACAT
CATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATTGTACAGAAATATGC
TTCTCTGGGATCACTCTATGATTACATTAAACAGTAACAGAAGTGAGGAGATGGATATGGA
TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
TCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAA CATAACAACACACATGTC
CTTGGTTGGAACCTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTGTCAGA
AACTTGTGACACATATTCTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
CTTTAAAGGTTTGGAAAGGATTACAAGTAGCTTGGCTTGTAGTGGAACAAAAACGAGAGATT
AACCATTCCAAGCAGTTGCCCCAGAAGTTTGTCTGAAGTGTACATCAGTGTGGGAAGC
TGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCATCCTGGAGTCCATGTCAAA
TGACACGAGCCTTCTTGACAAGTGTAACCTATTCCTACACAACAAGGCGGAGTGGAGGTG
CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGATCTCAGCTTTAAGGA
GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAAGCTGACAGAGCA
GTCCAACACCCCGCTTCTCTTGCCTCTTGCTGCAAGAATGTCTGAGGAGTCTTACTTTGA
ATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTCTGTGATCACAGCAACAAGTAA
CGGGGAGGGCCATGGCATGAACCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
AGCCAAGCAGAATTCTTCCAAAACCATCTAAGAGAAGGGGGAAGAAAGTCAACATGGC
TCTGGGGTTTCAAGTATTTTGAAGTGTGACGATGATGATGATGATGACGGTGA
GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
CAAATGTTTGGAAAACACAAAAGTAACCTGTTTATCTCAGTCTGTACAAAAACAGTAAGG
AGGCAGAAAGCCAAGCACTGCATTTTTTAGGCCAATCACATTTACATGACCGTAATTTCTT
ATCAATTCTACTTTTTATTTTTTGCTTACAGAAAAACGGGGGGAGAATTAAGCCAAAGAAGT
ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
ATAGGACTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAAATGAATACTTTTTTAGTTTG
TATTTGACTTTATTTCTTTTATTCAAATCATTTTTAAAACTTACATTTTGAACAAACAC
TCTTAACCTCTAATTGTTCTTTGACACGTAAGTAACTCTGTGACATACTTTTTTTTTCTTA
TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
TACTAATAATTAAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTTGG
GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
GATGGCACCCTGCACTCTAGCCTGGGCAAGAGAACAGATCCTGTCTCAAAAAACAAAA
AAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLPFFENC GGGSFGSVYRAKMWISQDKEVAVK
KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDM
HIMTATDVAKGNHYLHNEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTHMS
LVGTFPMMAPEVIQSLFVSETCDTYSYGVVLMENLTREVFPKGLEGLQVANLVVEKNERL
TIPSSCFRSPFAELLHQWEADAKRPSFKQIIISLESMSNDTSLPDKNSPLHNKAEMRC
EIEATLERLKKLERDLSFKQELKERERRLKMWEQKLTQSNTPLLLPLAARMSEESYFE
SKTEESNSAEMSCQITATSNGEHGNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQ
AKQNSSKTTSKRRGKKNMALGFSDFDLSEGGDDDDDDGEEEDNDMENSE

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGCACCGGGCCGCGGCGCCACCATGGCCGTGC
GACAGGCGCTGGGCGCGCGGCTGCGAGCTGGGTGAGCGCTGCTGCTGCGCTTCACGGGCA
AGCCCGGCGGGCCTACGGCTTGGGGCGGCGGCGGGCCCGGCGGCGGGCTGTGTCCGCGGGG
AGCGTCCAGGCTGGGCGCGCAGGACCGGGCGCGGAGCCTCGCAGGGTGGGGCTCGGGCTTC
CTAACCGTGTCCGCTTCTTCCGCCAGTCCGGTGGCCGGGCTGGCGGCGCGGTTGCGAGCGGC
AGTTCTGTGGTGGCGGCTGGGGCTGCGCGGGCCCTTGGCGGCGGGCAGTCTTTCTGGCCT
TCGGGCTAGGGCTGGGCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGG
CCTGTGAGGAGATCCAGGCAATTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGG
ACACGAGACGCTTGCAGGGCTTTCCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
AGGGCTGCGAGTGTCTGTGTATGAAGCCACCATGCGCTACATTGCCCCAGAACCTGGAGG
TGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGCCAGGTACAGTGCACAGGAGAAG
GGCAGGAGCGAGCTCCGGGGGCCCCCTGCGCTTCCCTTGGCCATCAAGATGATGTGGAACA
TCTCGGCAGGTTCTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
CGAGCCGAGTGGCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAG
GTCCCAAGCAACTAGCCCCCTCACCCCAACATCATCCGGGTTCTCCGCGCTTCACCTCTT
CCGTGCGCGCTGCTGCCAGGGGCCCCCTGGTGGAGTACCCTGATGTGCTGCCCTCACGCTCC
ACCCTGAAGGCTGGGCCATGGCCGGACGCTGTTCCTCGTTATGAAGAACTATCCCTGTA
CCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCCGCCTCGCGCCATGATGCTGC
TGCAGCTGTGGAAGGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCTGGCTGGTGATCGCAG
ATTTTGGCTGTGCTGGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGT
ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTGT
GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCT
ATGAAATCTTCGGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCC
GCAGCTACCAAGAGGCTCAGTACCTGCAGTACCTGCGAGAGAGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
CAAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAACTGAAGT
TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
TCACAGAGAAGTGTGTGTGGAAACAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGT
GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTCTGTGATGGTCTG
TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
AAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAAGTGAAGTTCAGTCTGCAGTCTCTGTC
TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAG
TTTGGCTGTGACCTTTGCCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATG
TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTGAGCAGTTCAGTTACGGG
AGTGGGAAATTACATGAGGCTGGGCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGC
TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTGAATAT
GGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAATAT
TAAATGCAAAATTTACAACCTGCAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCCC

FIGURE 3

Met Ala

Val	Arg	Gln	Ala	Leu	Gly	Arg	Gly	Leu	Gln	Leu	Gly	Arg	Ala	Leu	Leu	5	10	15	
Leu	Arg	Phe	Thr	Gly	Lys	Pro	Gly	Arg	Ala	Tyr	Gly	Leu	Gly	Arg	Pro	20	25	30	
Gly	Pro	Ala	Ala	Gly	Cys	Val	Arg	Gly	Glu	Arg	Pro	Gly	Trp	Ala	Ala	35	40	45	50
Gly	Pro	Gly	Ala	Glu	Pro	Arg	Arg	Val	Gly	Leu	Gly	Leu	Pro	Asn	Arg	55	60	65	
Leu	Arg	Phe	Phe	Arg	Gln	Ser	Val	Ala	Gly	Leu	Ala	Ala	Arg	Leu	Gln	70	75	80	
Arg	Gln	Phe	Val	Val	Arg	Ala	Trp	Gly	Cys	Ala	Gly	Pro	Cys	Gly	Arg	85	90	95	
Ala	Val	Phe	Leu	Ala	Phe	Gly	Leu	Gly	Leu	Gly	Leu	Ile	Glu	Glu	Lys	100	105	110	
Gln	Ala	Glu	Ser	Arg	Arg	Ala	Val	Ser	Ala	Cys	Gln	Glu	Ile	Gln	Ala	115	120	125	130
Ile	Phe	Thr	Gln	Lys	Ser	Lys	Pro	Gly	Pro	Asp	Pro	Leu	Asp	Thr	Arg	135	140	145	
Arg	Leu	Gln	Gly	Phe	Arg	Leu	Glu	Glu	Tyr	Leu	Ile	Gly	Gln	Ser	Ile	150	155	160	
Gly	Lys	Gly	Cys	Ser	Ala	Ala	Val	Tyr	Glu	Ala	Thr	Met	Pro	Thr	Leu	165	170	175	
Pro	Gln	Asn	Leu	Glu	Val	Thr	Lys	Ser	Thr	Gly	Leu	Leu	Pro	Gly	Arg	180	185	190	
Gly	Pro	Gly	Thr	Ser	Ala	Pro	Gly	Glu	Gly	Gln	Glu	Arg	Ala	Pro	Gly	195	200	205	210
Ala	Pro	Ala	Phe	Pro	Leu	Ala	Ile	Lys	Met	Met	Trp	Asn	Ile	Ser	Ala	215	220	225	

FIGURE 3 (cont'd)

Gly	Ser	Ser	Ser	Glu	Ala	Ile	Leu	Asn	Thr	Met	Ser	Gln	Glu	Leu	Val	230	235	240
Pro	Ala	Ser	Arg	Val	Ala	Leu	Ala	Gly	Glu	Tyr	Gly	Ala	Val	Thr	Tyr	245	250	255
Arg	Lys	Ser	Lys	Arg	Gly	Pro	Lys	Gln	Leu	Ala	Pro	His	Pro	Asn	Ile	260	265	270
Ile	Arg	Val	Leu	Arg	Ala	Phe	Thr	Ser	Ser	Val	Pro	Leu	Leu	Pro	Gly	275	280	285
Ala	Leu	Val	Asp	Tyr	Pro	Asp	Val	Leu	Pro	Ser	Arg	Leu	His	Pro	Glu	295	300	305
Gly	Leu	Gly	His	Gly	Arg	Thr	Leu	Phe	Leu	Val	Met	Lys	Asn	Tyr	Pro	310	315	320
Cys	Thr	Leu	Arg	Gln	Tyr	Leu	Cys	Val	Asn	Thr	Pro	Ser	Pro	Arg	Leu	325	330	335
Ala	Ala	Met	Met	Leu	Leu	Gln	Leu	Leu	Glu	Gly	Val	Asp	His	Leu	Val	340	345	350
Gln	Gln	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Ile	Leu	Val	355	360	365
Glu	Leu	Asp	Pro	Asp	Gly	Cys	Pro	Trp	Leu	Val	Ile	Ala	Asp	Phe	Gly	375	380	385
Cys	Cys	Leu	Ala	Asp	Glu	Ser	Ile	Gly	Leu	Gln	Leu	Pro	Phe	Ser	Ser	390	395	400
Trp	Tyr	Val	Asp	Arg	Gly	Gly	Asn	Gly	Cys	Leu	Met	Ala	Pro	Glu	Val	405	410	415
Ser	Thr	Ala	Arg	Pro	Gly	Pro	Arg	Ala	Val	Ile	Asp	Tyr	Ser	Lys	Ala	420	425	430

FIGURE 3 (cont'd)

Applicant: Acton, Susan L.
Title: NOVEL PROTEIN KINASE MOLECULES AND USES
THEREFOR
Attorney/Agent: Tracy M. Sioussat
Docket No.: MPI1998-052PIRDV10DVIM
Sheet 8 of 11 Sheets

Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val
435 440 445 450

Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
455 460 465

Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
470 475 480

Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
485 490 495

Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
500 505 510

His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
515 520 525 530

Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
535 540 545

Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
550 555 560

Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
565 570 575

Ala Ala Leu

GTCGACCCACGCGGTCCGCCCCACGCGTTCCGGAGACATGTCTCTGTGTTTC
TCTCCCCCTCCGCTTTTGAGTCCGTTGAAGACACAATTTCTCTCTGTGCGGT
GCTTAGGAGGAGCTCCATGAACATGTATTGAATTGGACTTAGCTGAACAG
GCTGCTGGTTGGCTGCCCAGAGGGGGCAGGCTGTGTTGCTGGGAGCCTTC
CAGCTCCCTGCAGCAGTCATGGGGCAGGGTTCCCCGAGTCCGTAATCCCC
ATTTCCACCTACTTTCCCTTAGTTATTTGATTCCCTGTCTGTCTGTAATCAGC
TTAAGTGGAGCATCCCCCTTTCCTGGGAGACACGAAGCAGGAAACACTGGC
AAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTCTTCAGCCAGA
CGAGCGAGCTGGCCAAGGACTTTATTCGGAAGCTTCTGGTTAAAGAGACC
CGGAAACGGCTCACAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCC
GGTGGACAACCAGCAAGCCATGGTGCAGCAGGGAGTCTGTGGTCAATCTGG
AGAACTTCAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTTCCTTCAGC
ATCGTGTCCCTGTGCAACCACCTCACCCGCTCGCTGATGAAGAAGGTGCA
CCTGAGGCCGGATGAGGACCTGAGGAACTGTGAGAGTGACACTGAGGAG
GACATCGCCAGGAGGAAAGCCCTCCACCCACGGAGGAGGAGCAGCACCT
CCTAACTGGCCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCACGCGG
GGCTCCCTTCTGTGCAGACTTTTGGACCCAGCTCAGCACCCAGCACCCGGG
GTCCTGAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAAGAGCTT
GCAGGCAAGCCAGGAGACCCTGGGAGCTGTGGCTGTCTTCTGTGGAGGAG
GCTCCAGCATTCCCAAAGCTCTTAATTCTCCATAAAATGGGCTTTCCTCTG
TCTGCCATCCTCAGAGTCTGGGGTGGGAGTGTGGACTTAGGAAAACAATA
TAAAGGACATCCTCATCATCACGGGGTGAAGGTCAGACTAAGGCAGCCTT
CTTCACAGGCTGAGGGGGTTCAGAACCAGCCTGGCCAAAAAATTACACCAG
AGAGACAGAGTCCTCCCCATTGGGAACAGGGTGATTGAGGAAAGTGAACC
TTGGGTGTGAGGGACCAATCCTGTGACCTCCCAGAACCATGGAAGCCAGG
ACGTCAGGCTGACCAACACCTCAGACCTTCTGAAGCAGCCCATTGCTGGC
CCGCCATGTTGTAATTTTGCTCATTTTTATTAACTTCTGGTTTACCTGATG
CTTGGCTTCTTTTAGGGCTACCCCCATCTCATTTCCTTTAGCCCGTGTGCCT
GTAACCTCTGAGGGGGGGCACCCAGTGGGGTGTGAGTGGGCAGAATCTCA
GAAGGTCCTCCTGAACCGTCCGCGCAGGCCTGCAGTGGGCCTGCCTCCTC
CTTGCTTCCCTAACAGGAAGGTGTCCAGTTCAAGAGAACCCACCCAGAGA
CTGGGAGTGGTGGCTCACGCCTATAATCCCTGCGCTTTGGCAGTCCGAGG
CAGGGGAATTGCTTGAACCTCAGGAGTTGGAGACCAGCCTGGGCAACATGG
CAAAACGCAGTCTGTACAAAAAATACAAAAAATTAGCCAGGTGTAGGGGT
AGGCACCTGGCATCCCAGCTACTCCAGGGGCTGAGGTGACAGCATTGCTT
AAGCCCAGAAGGTGAGGCTGCAGTGAGCTGAGATCACGCCACTGCACTC
CAGTCTGGGTGACAGAGAGAGACCATATCCAAAAAAGGG
CGGCCGC

LFDSLVSVLSLSGASPFLGDTKQETLANITAVSYDFDEEFFSQTSELAKDFIRKL
LVKETRKRLTIQEALRHPWITPVDNQAMVRRESVNVLENFRKQYVRRRWK
LSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRSSTS

FIGURE 4

Applicant: Acton, Susan L.

Title: NOVEL PROTEIN KINASE MOLECULES AND USES THEREFOR

Attorney/Agent: Tracy M. Sioussat

Docket No.: MPI1998-052PIRDV10DV1M

Sheet 10 of 11 Sheets

T A L A K E L R E L R I E E T N R P M 19
G A G C A T T A G C C A A G A A C T A A G A A C T C C G A T T G A A G A A C A A C C C C A A T G 57
K K V T D Y S S S S B E S E S S E E E E 39
A A G A A G G T G A C T G A T T A C T C C T C C A G T G A G G A G T C A G A A A G T A O C G A G G A A G A G G A G 117
E D G E S E T H D G T V A V S D I P R L 59
G A A G A T G A G A G A G C G A G A O C C A T G A T G G G A C A G T G C T G T C A G C A T A C C A G A C T G 177
I P T G A P G S N E Q Y N V G M V G T H 79
A T A C C A C A G G A G C T C C A G C A G A A C G A G C A G T A C A A T G T G G A A T G G T G G G A O C C A T 237
G L E T S H A D S F S G S I S R E O T L 99
O G G C T G G A G A O C T C T C A T G O G G A C A G T T T C A G C G C A G T A T T T C A A G A G A A C C A T T G 297
M I R E T S G E K K R S G H S D S N G F 119
A T G A T T A G A G A G A C G T C T G A G A A G A A G C A T T C T G C C A C A G T G A C A C C A A T G C C T T T 357
A G H I N L P D L V Q Q S H S P A G T P 139
G C T G C C A C A T C A A C C T C C T G A C C T G G T G C A G C A G A O C C A T T C T C C A G C T G A A C C O G 417
T E G L G R V S T H S Q E M D S G T E Y 159
A C T G A G G A C T G G G C G C G T C T C A A C C A T T C C C A G G A G A T G G A C T C T G G G A C T G A A T A T 477
G A G S S T K A S F T P F V D P R V Y Q 179
G O C A T G G G A G C A C C A C C A A G C C T T C A C C C C T T T G T G G A C C C C A G A G T A T A C C A G 537
T S P T D E D E D E S S A A A L F T 199
A G T T C T C C C A C T G A T G A A G A G G A T G A G G A A T C A T C A G C C A G C T C T G T T T A C T 597
S E L L R O E Q A K L N E A R K I S V V 219
A G C G A A C T T C T T A G G C A A G A A C A G C A A C C A A C A G A A A G A A T T T O G G T G G T A 657
N V N P T N I R P H S D T P E I R K Y K 239
A A T G T A A A C C A C C A A C A T T C O G C T C A T A C C G A C A C A C A G A A A T C A G A A A A T A C A A G 717
K R F N S E I L C A A L W G V N L L V G 259
A A A C A T T C A C T C A G A A A T A C T T G T G C A G C T C T G G G T G T A A A C C T T C T G G T G G G 777
T E N G L M L L D R S G Q G K V Y N L I 279
A C T G A A A A T G C C T G A T G C T T T G C A C A G T G G C C A A G C C A A G T C T A A T A T C T G A T C 837
N R R R F Q Q M D V L E G L N V L V T I 299
A A C C O G A O G C G A T T T C A G C A G A T G G A T G T G C T A G A G G A C T G A A T G T C C T T G T G A C A A T 897
S G K K N K L R V Y Y L S W L R N R I L 319
T C A G A A A G A A G A A T A A G C T A C G A G T T T A C T A T C T T T C A T G G T T A A G A A C A G A A T A C T A 957
H N D P E V E K K Q G W I T V G D L E G 339
C A T A A T G A C C C A G A G T A G A A A G A A A C A A G C C T O G A T C A C T G T T G G G A C T T G G A A G C 1017
C I H Y K V V K Y E R I K F L V I A L K 359
T G T A T A C A T T A A G T T A A T G A A A G A T C A A A T T T T T G G T G A T T G C C T T A A A G 1077
N A V E I Y A W A P K P Y H K F M A F K 379
A A T C T G T G A A A T A T G C T T G G C T C T A A A C C G T A T C A T A A A T T C A T G C A T T T A A G 1137
S F A D L Q H K P L L V D L T V E E G Q 399
T C T T T G C A G A T C T C C A G C A C A A G C T C T A G T T G A T C T C A C G G T A G A A G A A G G T C A A 1197
R L K V I P G S H T G F H V I D V D S C 419

FIGURE 5

AGA TTA AAG GTT ATT TTT GGT TCA CAC ACT GGT TTC CAT GTA ATT GAT GTT GAT TCA GGA 1257
N S Y D I Y I P S H I Q G N I T P H A I 439
AAC TCT TAT GAT ATC TAC ATA CCA TCT CAT ATT CAG GGC AAT ATC ACT OCT CAT GCT ATT 1317
V I L P K
GTC ATC TTG CCT AAA 444
1332

FIGURE 5 (cont'd)